

A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular and
A:Reference number: A35356; MUID:90260639
A:Accession: A35356
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <SM1>
A:Cross-references: GR:M32315; NID:q189185; PIDN:AAA59929.1; PID:q189186
R:Kobayashi, H., Hata, K., Sakata, S., Schwart, P. F., King, M.W., Hata, K.K., Squires,
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occur-
A:Reference number: A36475; MUID:91045991
A:Accession: A36475
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-195, 'P', 197-461 <K08>
A:Cross-references: GB:M55994; GB:M48549; NID:q339757; PIDN:AAA36755.1; PID:q339758
R:Dembic, Z., Loetscher, H., Gubler, U., Pan, Y.C., Lamm, H.W., Geulz, R., Brockhaus, M.,
Cytokine 2, 231-237, 1990
A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular,
A:Reference number: A48416; MUID:91370690
A:Accession: A48416
A>Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 23-461 <DEM>
A:Cross-references: GR:S3368; NID:q33648; PIDN:AAR19824.1; PID:q33649
A:Note: sequence extracted from NCI backbone (NCBI:63368; NCIPI:63371)
R:Heller, P. A., Song, K., Quasch, M.A., Fischer, W.H., Chang, D., Ringold, P.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demon-
A:Reference number: A36007; MUID:90349572
A:Accession: A36007
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 116-140, 'P', 142-195, 'P', 197-362, 'T', 364-461 <HEL>
A:Cross-references: GR:M36857; NID:q339751; PIDN:AAA63262.1; PID:q339752
R:Loetscher, H., Schliesser, E.J., Lamm, H.W., Pan, Y.C.F., Lesslauer, W., Brockhaus, M.,
J. Biol. Chem. 265, 20311-20318, 1990
A:Title: Purification and partial amino acid sequence analysis of two distinct tumor nec-
A:Reference number: A3666; MUID:q1056048
A:Accession: A3666
A>Status: preliminary
A:Molecule type: protein
A:Residues: 23-40; 65-69, 136-141; 400-406 <LOS>
R:Engelmann, H., Novick, D., Wallach, D.,
J. Biol. Chem. 265, 1531-1536, 1990
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A:Reference number: A35010; MUID:90110215
A:Accession: A35010
A>Status: preliminary
A:Molecule type: protein
A:Residues: 27-31 <ENG>
R:Kühnert, P., Kemper, O., Wallach, D.,
Gene 150, 381-386, 1994
A:Title: Cloning, sequencing and partial functional characterization of the 5' region of
A:Reference number: 138094; MUID:95121944
A:Accession: 138094
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-37 <RES>
A:Cross-references: FMBL:X80021; NID:q666044; PIDN:CAA56324.1; PID:q825701
C:Genetics.
A:Gene: GDB:TNFR2
A:Map position: lp36.2-1p36.2
A:Introns: 26/3
A:Note: the list of introns is incomplete
C:Superfamily: Tumor necrosis factor receptor type 2; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-22/Domain: signal sequence status: predicted <SIG>
F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
F:40-76/Domain: NGF receptor repeat homology <NH>
F:78-119/Domain: NGF receptor repeat homology <NC2>
F:120-162/Domain: NGF receptor repeat homology <NC3>

F:164-291/Domain: NGF receptor repeat homology <NC4>
F:262-279/Domain: transmembrane #status predicted <MN>
F:280-461/Domain: intracellular #status predicted <INT>
F:171,193/binding site: carbohydrate (asn) (covalent) #status predicted

alignment_scores:
Quality: 204.00 Length: 422
Ratio: 1.074 Gaps: 21
Percent Similarity: 45.024 Percent Identity: 24.645

alignment_block:
US-09-525-998A-1 x A35356

Align seq 1/1 to: A35356 from: 1 to: 461

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124 AGTGTGTGTCGCGCAAGAAATAATATACACGCTCAAAATAATATGATTTG 173
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
38 SerThrCysArgLeuArgGluTyr...TyrAspGlnThrAlaGlnMetCys 53
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
174 CTGTACCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 223
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
53 CysSerLysCysSerProGlyGlnHisAlaLysValPheCysThr...L 69
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
224 CGCGCCAGCATACGACATCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 273
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
69 ysthrSerAspThrValCysAspSerCysGlnAspSerThrThrThrGln 85
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
274 TCAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 320
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
86 LeuTrpAsnTrpValProGluCysLeuSerCysCysArgCysSerSer 102
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
321 GAAATGGGTAGGTGAGAGATCTTCTTCAAGAGAGAGAGAGAGAGAGAGAG 370
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
192 Asp...GlnValGlnThrGlnAlaCysThrArgGlnGlnAspArgI 117
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
371 TGTGTGCTCAGCAGAGAACCACTACCGGATATATGGAGAGAGAGAGAGAG 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
117 LeuCysThrCysArgProGly...TrpTyrCysAlaLeu 128
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
421 TGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 470
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
129 SerLysGlnGluCysArgGluCysAla... 138
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
471 CTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 520
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
139 ...ProLeuArgLysCysArgProGlyPheGly 149
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
521 TA...ACAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 555
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
149 AlaAlaArgProGlyThrGlnThrSerAspValValCysLysProCysAla 165
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
556 ...AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 591
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
166 ProGlyThrPheSerAspThrThrSerSerThrAspLysCysArgProH 182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
692 CAATTGGAAGATTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 640
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182 GlnAlaCysAsnVal...ValAlaI 190
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641 GCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 690
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
190 LePro... 191
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
691 GGTTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 740
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192 ...GlyAsnAlaSerMetAspAlaVa 199
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741 TTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 790
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199 LysThrSerThrSerPro... 206
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791 CTAGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
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206 hArqSeMeAlaProGlyAlaValHisLeuProGlnProValSerThr 222
841 CCAACCTGGGTTTCAGTCCGCGCCAGAGT...GCCACCTTCACCTCCAG 887
223 ArqSerGlnHisThrGlnProThrProGlnProSerThrAlaProSerTh 239
888 CTCACCTATACCCCT...AGGACAGCTGC 913
239 rSerLeuLeuLeuProMetGlyProSerProProAlaGlySerThrG 256
914 CCAATTTGGGCTTGGGATGAGAGAGTGGTAAAGAGGATACAGAGGGGCT 963
256 LyAspPheAlaLeuProValGlyLeuLeuValGly...ValThrAla 270
964 CACCCATCTTTCGCACAGCCCTCGCTCCGACCCGATGCCAACCCCT 1013
271 LeuGlyLeuLeuLeuLeuGlyValValAlaSerCysValLeuLeuThrGlnVa 287
1014 TAAAGATGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1062
287 HisLys...LysProLeuCysLeuGlnArgGlnA 298
1063 A...GCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1097
298 LaLysValProHisLeuProAlaAspLysAlaArg...GlyThrGln 312
1098 GCGCCCTTGGCGTGGAGAAATTCCTCCGCGCTAGCGCTCAGCGCAC 1147
313 GlyProGlnGlnHisLeuLeuLeuThrAlaProSerSerSerSe 329
1148 AGGA...GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1194
329 rSerLeuGluSerSerAlaSerAlaLeuAspArgArgAlaProThrArg 346
1195 GGCAATATATATATATATATATATATATATATATATATATATATAT 1244
346 sGlnProGlnAlaProGly ValGlnAla... 355
1245 GGTATATATATATATATATATATATATATATATATATATATATAT 1294
356 .....SerGlyAlaGlyGlnAlaArgAlaSerThrGlySerSerAspSe 370
1295 GGTGCTGGAGAGCAT 1310
370 rSerProGlyGlyHis 375

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seq_name: pirl:G0V2ML

seq_documentation_block:

12 protein : myxoma virus (strain Lausanne)

C:Species: myxoma virus

C:Date: 31 Dec 1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999

C:Accession: A40566

R:Upton, C.; Macen, J.L.; Schreiber, M.; McLadden, G.

Virology 184, 370-382, 1991

A:Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis factor

A:Reference number: A40566; M01D:91335768

A:Molecule type: DNA

A:Residues: 1-326 <FTS>

A:Cross-references: GB:M95181; GB:M79276; NID:q12259; PID:AAA45632.1; FID:q122410

C:Superfamily: myxoma virus T2 protein, NGF receptor repeat homology

C:Keywords: glycoprotein

F:64-105, 64-107 NGF receptor repeat homology NC2

F:106-147/Domain: NGF receptor repeat homology <NG3>

F:66,181,205,219/Binding site: carbohydrate (Asn) (covalent) #status predicted

alignment_scores:

Quality: 200.00 Length: 240

Ratio: 1.695 Gaps: 10

Percent Similarity: 49.167 Percent identity: 25.833

alignment_block:

US-09-525-998a-1 x G0V2ML

Align seq 1/1 to G0V2ML from: 1 to: 326

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40 GTGTCCTGAGATGTTGGTGGAAATATAGCGTTCARBBGHTATIGGACI 89
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6 LeuLeuLeuAlaValValAlaCysValGlyGlyGly 18
90 GGTCCCTCAGATACAGGACAGGACAGACAGATACAGTGGTGGCCCAA 149
||||| ||||| ||||| ||||| |||||
19 AlaProGlyGlyAlaAspArgGlyLys...CysArgGlnVa 31
140 GAAATATATATACGCTCAAAAATAATTCGATTGCTGATCAATGGCAT 189
||| ||| ||||| ||||| ||||| ||||| |||||
31 SerAspLys...GlnLysAspGlyGlyGlyCysThrSerCysPro 44
190 AAGAGACCTACTGTATCAATGACTGTCCAGGGGCGGAGGATATAGGA 249
||||| ||||| ||||| ||||| |||||
45 ProGlySerLysThrAlaSerArgLeuCys...GlyProGlySerAspThrVa 60
240 CAGCAGCCAGCTCAGACGCGCTGCTTCACGCTTCACAAAAACACCTCA 289
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60 LysSerProGlyLysAspGlnThrPheThrAlaSerThrAsnHisAla 77
290 CACACTTCCTCAGCTGC...GCCAAATGCGCAACGAAATCGCTCACTG 346
||||| ||||| ||||| ||||| ||||| |||||
77 rAlaCysValSerCysArgGlyArgCysThrGlyHisLeuSer... 91
337 GAGATCTCTTTGATAGTGGAGGGGAGACAGGTGTGTGCTTCAGAAA 406
||||| ||||| ||||| ||||| ||||| |||||
92 GluSerGlnSerCysAspLysThrArgAspArgValCysAspLysSerAl 108
387 CAACCAAGAA... 396
108 aGlyAsnThrCysLeuLeuLysGlyGlnGlyGlyCysArgLysCysAlaP 125
396 ..... 396
125 rGlySerThrCysProAlaGlyThrGlyValSerGlyHisThrArgThr 141
397 .....CGCATATTGGAGTAAAAACT 419
||||| ||||| ||||| ||||| ||||| |||||
142 GlyAspValLeuCysThrLysCysProArgThrLysSerAspAlaVa 158
420 TTTCACAGCTTCATTCACGCTGCTCAATGGG...AGGAGGACG 466
||| ||| ||||| ||||| ||||| ||||| |||||
158 LysSerThrGluThrCysThrSerSerPheAsnLysLysSerValGlnP 175
467 TCCTGCTCAGAGAACACACACACACACGCTGCTGCTGCTGCTGCTG 516
||||| ||||| ||||| ||||| ||||| |||||
175 LeuSerGlyThrValAspArgSerCysThrThrThrAlaThr... 190
517 TTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 566
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191 .....PheAspGlnValValCysThrSerGlnGlnSerValThrLe 204
567 G...GAGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 607
||||| ||||| ||||| ||||| ||||| |||||
204 AsnSerThrAspCysAspProValPheHisThrGluThrGlyThrGly 621
608 AGGCACTGAGACACTCAGCT 627
||||| ||||| ||||| ||||| ||||| |||||
221 GCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 627
seq_name: pirl:G0V2ML

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seq_documentation_block:

nerve growth factor receptor, low affinity precursor - chicken

N:Alternate names: NGF receptor

C:Species: Gallus gallus (chicken)

C:Date: 10 Sep 1992 #sequence_revision 10-Sep-1992 #text_change 10-Sep-1999

C:Accession: JN0006; A60504
 R:Larac, T.H.; Weiskamp, G.; Helder, J.C.; Padoke, M.J.; Misko, T.P.; Shooter, E.M.; Reif, Neuron 2, 1123-1134, 1994
 A:Title: Structure and developmental expression of the nerve growth factor receptor in d
 A:Reference number: JN0006; MUID:90166579
 A:Accession: JN0006
 A:Molecule type: mRNA
 A:Residues: 1-416 <LAR>
 A:Experimental source: embryonic chick brain
 R:Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, E.F.; Bothwell, M. Dev. Biol. 137, 287-304, 1990
 A:Title: Structure and developmental expression of the chicken NGF receptor.
 A:Reference number: A60504; MUID:90152140
 A:Accession: A60504
 A:Status: preliminary, not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 21-35, 97, 37-172, 174-275, 277-495, 497-539
 C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c
 C:Comment: The cysteine rich region of the extracellular domain may form part or all of
 C:Comment: This protein is thought to form a high-affinity receptor when it associates w
 C:Superfamily: nerve growth factor receptor, NGF receptor repeat homology
 C:Keywords: duplication, glycoprotein, heterodimer, monomer, phosphoprotein, receptor; d
 F:1-29/Domain: signal sequence status predicted <SIG>
 F:21-416/Product: nerve growth factor receptor #status predicted <MAT>
 F:21-239/Domain: extracellular #status predicted <EXT>
 F:24-57/Domain: NGF receptor repeat homology <NG1>
 F:59-100/Domain: NGF receptor repeat homology <NG2>
 F:101-139/Domain: NGF receptor repeat homology <NG3>
 F:141-181/Domain: NGF receptor repeat homology <NG4>
 F:189-247/Region: serine/threonine-rich
 F:240-261/Domain: transmembrane #status predicted <MEM>
 F:262-416/Domain: intracellular #status predicted <INT>
 F:52/Binding site: carbohydrate (Asn) (covalent) #status predicted

alignment_scores:

Quality	197.50	Length	489
Ratio	0.890 <td>Gaps</td> <td>32</td>	Gaps	32
Percent Similarity	45.399 <td>Percent Identity</td> <td>23.926</td>	Percent Identity	23.926

alignment_block:

US-09-525-998a-1 x JN0006

Align seq 1/1 to: JN0006 from: 1 to: 416

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31 CTGCCACATGCGTCCTCTCCACCTGCTGCTGGGGAATATACGCTCAGCGGT 80
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5 ValProLeuLeuLeuLeu.....LeuLeuProAlaGly.. 15

81 TATTGGATGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 130
   |||||
16 .....ProThrTrpGlySerGlyGlyGly.....C 24

141 GTCCCAAGGAAATATATCATCATCATCATCATCATCATCATCATCATCAT 180
   |||||
24 ValLeuThrLysMetTyr.....ThrThrSerGlyGlyCysLys 37

181 AAGTCCACAAAGCAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 230
   |||||
38 AlaCysAsnLeuGlyGlyGlyValValGlnProCys...GlyValAsnGln 53

241 GATATACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 277
   |||||
53 .....ThrValCysGlnProCysLeuAspSerValThrThrSerAspThr 69

278 AAAATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 327
   |||||
69 ValSerAlaThrGlnProCysLysProCysThrGlnCys.....Val 82

328 GGTACAGTCGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 374
   |||||
83 GlyLeuIleSerMetSerAlaProCysValGlnSerAspAlaValCys 99

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375 TGGTCTGTAGAAAGAAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 424
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99 sarGlys.....AlaIleGlyTrpIleGlyGlyAspGlyGlySerGlyGly 113

425 AGTCTCTCAATTCGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 471
   |||||
113 erCysLysGlyCysSerIleCysGlyValGlyPheGlyLeuMetPhePro 129

472 TCCAGAGAGAAACAGAACACACGCTCTCTCTCTCTCTCTCTCTCTCTCT 518
   |||||
130 CysArgaspSerGlnaspThrValCysGlyCysProGlyGlyThrPhe 146

519 TCTAAGAGAA.....AAGCAGTGTGTCTCTCTCTCTCTCTCTCTCTCT 556
   |||||
146 eSerAspGluAlaAsnPheValAspProCysLeuProCysThrIleCysG 163

557 AGAAAGGCTGTAGTACACCAACATCTCTCTCTCTCTCTCTCTCTCTCTCT 606
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163 LuGluAsnGluValMetValValGlyCys..... 172

607 AAGGGAATCTAGAGACACACACACACACACACACACACACACACACAC 656
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173 ThrAlaIleThrSerAspAlaGluCysArgaspLeuHisPro..... 185

657 CTCTGGCTTTCGCTTTTATCACTCTCTCTCTCTCTCTCTCTCTCTCTCT 706
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185 ..... 185

707 ACCAAGCTCTCAAGTCTCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 756
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186 .....ArgIleThrThrHisThrProSerLeu...AlaGlySerAspSer 199

757 CTCTCAAAAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 809
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200 ProGlu..... 205
   ProIleThrArg

807 AAATCTAAGCTCTAAGCTCTAAGCTCTAAGCTCTAAGCTCTAAGCTCTCA 856
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205 gAspPro...PheAsn...ThrGlyGlyMetAlaThrThrLeuAlaAsp 219

857 GTCCCGTCC.....CCAGTCTCCACCTCTCACTCTCTCTCTCTCTCTCT 885
   |||||
220 IleValThrThrValMetGlySerSerGlnProValValSerArgGlyTh 236

886 AGCTCCACCTATATCCCGCTGACCTCTCTCTCTCTCTCTCTCTCTCTCT 925
   |||||
236 rAlaAspAsnLeuIleProValThrCysSerThrLeuAlaValValVal 253

926 .....CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 958
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253 aGlyLeuValAlaIleThrIleAlaPheLysArgIlePAsnSerCysLys 269

959 GGCTGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1008
   |||||
270 AsnGlyGlnGlyAlaAsnAspArgProValAsnGlnThrProSerPro 286

1009 CCGCTTCTCAGA.....ACTCGGAG.....GACAGCG 1033
   |||||
286 uGlyGlnLysLysHisSerAspSerGlyIleSerValAspSerGlnSer 303

1034 CTTAT.....AAATTCACAGAGCTAGACACACACACACACACACACAC 1071
   |||||
303 euHisAspGlnGlnProProAsnGlnSerThrGlnGlyProAlaIlePro 319

1072 .....AATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1110
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320 GlyAspGlySerLeuThrAla.....SerLeuProProSerLysGln 333
   |||||
1111 .....TCTCAAGG 1117
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333 nGluGluValIleLysLeuLeuSerSerAlaGluGluThrThrTrpArg 350

1118 AATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1167

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[illegible]

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